

**FIG. 1**

**Multiple Alignment:**

### Multiple Alignment:

SPJ CA

SPJ  
CA

CA SPkinaseinHSDA59H18

SP) CAB62977

MEKPYAFTVHCVKRARRHRWKWAQVTFWCPEEQCHLWLQTLREMLEKLTSPKHLVFI  
-----PKHLVFI-----PKHLVFI-----PKHLVFI-----PKHLVFI-----

SP1 CA

SP] SPkinaseinHSDA59H18  
CA

CAB62977

NPFGGKGQCKRIYEEKVAPLFTLASITTDIGNKFFVNVYEVITEHANQAKETLYEINID  
NPFGGKGQCKRIYEEKVAPLFTLASITTDIGNKFFVNVYEVITEHANQAKETLYEINID

SPJ

SPJ SPkinaseinHSDA59H18

CA CAB62977

KYDGIWCVGGDMFSEVLHGLIGRTQRSAGVDQNHPRAVLWPSSLRIGLIPAGSTDCVCY  
KYDGIWCVGGDMFSEVLHGLIGRTQRSAGVDQNHPRAVLWPSSLRIGLIPAGSTDCVCY

CA  
[dS]

SPJ

SP kinase in F

STVGTSDAETSA LHI VVGDS LA MDVSS VHHNSTLLRYS VSLLGYG FYGDI IKDSEKKRWL  
STVGTSDAETSA LHI VVGDS LA MDVSS VHHNSTLLRYS VSLLGYG FYGDI IKDSEKKRWL

SPkinaseinHSDA59H18

CAB62977

GLARYDFSGLKTF LSHHCYEGT VSFLPAQHTVGSPRDRKPCRAGC FVCFQSKQOLEEE QK  
GLARYDFSGLKTF LSHHCYEGT VSFLPAQHTVGSPRDRKPCRAGC FVCFQSKQOLEEE QK

SPkinaseinHSDA59H18

CA B62977

KALYGLEAAEDVEEWQWVGKFLAINATNMSCARRSPGLSPAHLGDGSSDLILIRKC  
KALYGLEAAEDVEEWQWVGKFLAINATNMSCARRSPGLSPAHLGDGSSDLILIRKC

SPKinaseinHSDA59H18

CAB62977

SRFNFLRFLIRHTNQDQFD FT FVEVYRVKKFQFTSKHMEDESDLKEGGKKRFGHCSS  
SRFNFLRFLIRHTNQDQF-----

SPkinaseinHSDA59H18

CAB62973

HPSCCCTVSNSSWNCDEVLHSPAIEVRVHCQLVRLFARGIEENPKPDSHS

FIG. 2

Multiple Alignment:

```

S2180312      -----
A1237625      -----
SPkinaseinHSDA59H18  PKHLLVF INPFGGKGQGR IYERKVAPLFTLASITTD I GNKFYVNYVEVITEHANQAKE

S2180312      -----
A1237625      -----
SPkinaseinHSDA59H18  TLYEINI DKYDGI VCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPA

S2180312      -----
A1237625      -----
SPkinaseinHSDA59H18  GSTDCVCYSTVGTSDAETSA LHI VVGDSLAMDVSSVHHNSTLLRYSVSLGYGFYGDIIK

S2180312      -----
A1237625      -----
SPkinaseinHSDA59H18  DSEKKRWLGLARYDFSGLKTFL SHHCYEGTVSFLPAQHTVGSPRDRKPCRAGCFVCRQSK

S2180312      -----
A1237625      -----
SPkinaseinHSDA59H18  QQLEEEQKKALYGLEAAEDVEEWQVVC GKFLA INATNMSCACRRSPRGLSPA AHLGDGSS

S2180312      -----
A1237625      -----
SPkinaseinHSDA59H18  DLILIRKCSRNFRLRFLIRHTNQEDQFGFTFVEVYRVVKKFTQFTSKHVEDDNDLKELEKQ
DLILIRKCSRNFRLRFLIRHTNQDQFDFTFVEVYRVVKKFTQFTSKHVEDESDLKEGGKK

S2180312      -----
A1237625      -----
SPkinaseinHSDA59H18  KFGKICKDRPSC TCSASRSSWN CDGEV L HSPAIEVRVHCQLVRLFARGIEEES
KFGQICKDNPPCACTPSRSSWN CDGEV L HSPAIEVRVHCQLVRLFARGIEEES
RFGHICSHPSCCCTVSNSSWN CDGEV L HSPAIEVRVHCQLVRLFARGIEENPKPDSSH

```

FIG. 3

SPkinasemHSDA59H18	-----MEKPY-----AFTVHCVKRAKRWKWAQVT	
corrected_human_sphingosine	-----MDPAGGPRGVLPFC- <b>LVINFRGGKGEALQLFR</b>	C1
AF068748_EXT-2	-----MPPVCEPRGILLPC- <b>LVINFPQSGKGEALQLFR</b>	
Q06147	LYIDYKPHSS-SHLKEE-DDLVEFELKRSYKNTRENE-S <b>LVINFPFGGKGEAKKLFM</b>	
Q12246	LLIDHVSRSKRANTGEENISSGTVEELKKSYSKSKNE-S <b>LVINPHGGGTAKNLF</b>	
Q14159	CWVDFVENS-----QFCEYELVAYKGIKSE-F <b>LVINFPFGGKGEAKKLF</b>	
Q18425	CRSDAEENEQ-----LTSVLSRKPPPPQEQCGN <b>LVINFPNSSTFHSLETFA</b>	
SPkinasemHSDA59H18	FWCPPEQLCH-----LWLQTLREMLEKLTSPK-H <b>LVFINPFGGKGEAKKLF</b>	
corrected_human_sphingosine	SHVDFLAEEETSTIMLTER-----RNHARFLV <b>SEGRWDAIXVMFGDGLN</b>	C2
AF068748_EXT-2	SKVDFLEEEETFKLTER-----KNHARFLV <b>SEGRWDAIXVMFGDGLN</b>	
Q06147	TKAKFLLASRCIEVYTYKY-----PGHAIETAK <b>EDDEHYDTIACASGDGEF</b>	
Q12246	TKAKFLVESGCKIEVYTYKY-----ARHAIETAK <b>DDDEHYDTIACASGDGEF</b>	
Q14159	TEADPFSSSHSICDVTTER-----KDHAETAK <b>NDVGSVDGLISYGGDGLN</b>	
Q18425	NTGPKDKSLTRYDVVITG-----PNHAEVYVMT <b>KADEGKFNGLISYGGDGLN</b>	
SPkinasemHSDA59H18	RKHAFKFTLASITETTYGNLFFYVNVYEVITE <b>HANQAKETLYENIDKYDGLISYGGDGLN</b>	
corrected_human_sphingosine	<b>HEVHGLMERFD</b> WETAIQKPECSEFAGSGNAASIN <b>AGYEQVTNEDLTNTLL</b>	C3
AF068748_EXT-2	<b>HEVHGLMERFD</b> WETAIQKPECSEFAGSGNAASIN <b>AGYEQVTNEDLTNTLL</b>	
Q06147	<b>HEVHGLYQRPD</b> VKAFNNATTEPCGSGNAMS <b>CHNTN</b> NPSTY <b>STLLEK</b>	
Q12246	<b>HEVHGLYQRPD</b> VDAFNKLAATQPCGSGNAMS <b>CHNTN</b> NPSTY <b>STLLEK</b>	
Q14159	<b>HEVHGLGERDD</b> LEAFKLPFCMSEFAGSGNAF <b>SYN</b> AT <b>QLKPAETALEIK</b>	
Q18425	<b>FEAHNGECREDA</b> RIFFPTPLGIFSGSGNGL <b>LCVLSKYGT</b> TKMNEK <b>SVMERALEIA</b>	
SPkinasemHSDA59H18	<b>SEVHGLFGRQ</b> SAGVDQNHPRAVL <b>ESSLRIGTIPAGSTD</b> CVCYST <b>VGTSDAETSAH</b>	
corrected_human_sphingosine	L CRPVLSPMNLLSLHTASGLRS <b>SVLSAGFIADDESEYR</b> RLGEM <b>RFTLGTFLR</b>	C4
AF068748_EXT-2	L CRRRSPMNLLSLHTASGLRL <b>SVLSAGFIADDESEYR</b> RLGE <b>IRFTTGTFFR</b>	
Q06147	S IETRIDLMCCSQPSYAREHPK <b>SFLSQTGCIASDINTEFIR</b> WMGP <b>PAFELGVAFNI</b>	
Q12246	S IETRIDLMCCSQPSYMNWPR <b>SFLSQTGCIASDINTEFIR</b> WMGP <b>PFVFNLGAVFNI</b>	
Q14159	GRPISFDLMTFEQ---KGKKA <b>SFLFANYGFIADCDIGTNR</b> EMGEN <b>RAYLGFELRI</b>	
Q18425	TSPAKAESVALYSVKTDNQSY <b>SFLSGMGEMADIDSEEWKSL</b> GH <b>HEFTXMGFTS</b>	
SPkinasemHSDA59H18	I VVGDSLAMDVSSVHHNSTLLR <b>SVSLGFGFYGLIKSEKE</b> WLG <b>LARYDFSGLKTF</b>	
corrected_human_sphingosine	AALSTYRERLATLEVGTVGF-----ETP-----	
AF068748_EXT-2	ASLBITYOQLAYLEVGTVAS-----ETP-----	
Q06147	I QKKYPCIEYVKYAAKSKNELKNHYLEH <b>NGS</b> SLEFQHITMKNKDNE <b>CDNYNYENEYET</b>	
Q12246	I QKKYPCIEYVKYAAKSKNELKNHYLEH <b>NGS</b> SLEFQHITMKNKDNE <b>CDNYNYENEYET</b>	
Q14159	FQKPDWKSIEMDVVS SDRTIEKHMYE-----SK-----	
Q18425	CSLBSYKERLTYYRKYKPKGFHPSSNVFSVY <b>ET</b> -----TTQQRID---	
SPkinasemHSDA59H18	L SHHCYESTYSFLAQHTVGSPPD-----KKP-----CRAGCFVCR---	
corrected_human_sphingosine	-----ASPVVQVQ-----GPWDAHLVPLEEQ <b>PSHWQVVP</b> ---	
AF068748_EXT-2	-----ASTLVQK-----GPWDTHLVPLEEP <b>PSHWTVVP</b> ---	
Q06147	ENEDEDADADDEDSHLISRD <b>ADSSADQ</b> IKEDFKIKYPLDE <b>PSDWEREDPNIS</b>	
Q12246	S SPDLLSKNNINNSTKDE <b>SPNFLN</b> EDNFKLY <b>PPTEP</b> VEDW <b>EKMDS</b> ELT	
Q14159	-----N-----LAPMSES-----SDSDKT <b>VTSPE</b> SHLLT <b>FE</b> ---	
Q18425	-DSKVKTNGSVSDSEET <b>ETETKFN</b> -----WTLPDS <b>DETAVG</b> SSDLEET <b>VV</b> ---	
SPkinasemHSDA59H18	Q SKQQLLEEQKKALYGLEAAEDVEEWQV <b>CGKFLA</b> INATNMS <b>CACRRS</b> RG <b>LS</b> PA <b>AHLG</b>	
corrected_human_sphingosine	EDFVLVLALLH <b>HL</b> SKMFAP <b>MGRC</b> AA <b>VMHL</b> FYVRAG <b>VS</b> KA <b>ML</b> LR <b>FL</b> AM <b>EEGR</b> HEMEY	
AF068748_EXT-2	QDFVLVLVLLH <b>HL</b> SELFAAP <b>MGRC</b> EA <b>VMHL</b> FYVRAG <b>VS</b> RA <b>AL</b> LR <b>FL</b> AM <b>OK</b> GHMEI	
Q06147	NNLGIF <b>YTGKMPY</b> AA <b>DTKFFPA</b> AL <b>PSDGTMD</b> NV <b>TDART</b> SLTR <b>MAP</b> LL <b>GL</b> KG--SH <b>V</b>	
Q12246	DNLTF <b>YTGKMPY</b> AA <b>DTKFFPA</b> AL <b>PADGT</b> ED <b>LV</b> TD <b>ARIP</b> VTR <b>MTPE</b> LL <b>SL</b> KG--SH <b>V</b>	
Q14159	NDSL <b>FCAGLE</b> PY <b>APDA</b> KMFPA <b>SNDDGL</b> DE <b>VVYS</b> Q <b>FKS</b> LS <b>FT</b> Q <b>LN</b> NG--GF <b>Y</b>	
Q18425	DNFVN <b>YAVTL</b> HH <b>AA</b> DGP <b>FAPS</b> AK <b>LEDNR</b> HL <b>SYLW</b> DI <b>GTRVN</b> IA <b>KYLL</b> IA <b>IE</b> TH <b>IL</b>	
SPkinasemHSDA59H18	GSSD <b>KLIR</b> CK <b>ERFNF</b> LR <b>FLIR</b> HT <b>NQ</b> Q <b>Q</b> DF <b>TF</b> EV <b>YK</b> K <b>FQ</b> FT <b>SK</b> H <b>ED</b> ED <b>SD</b> LE <b>KEG</b>	
corrected_human_sphingosine	ECPVL <b>YYPV</b> AK <b>EL</b> EP <b>KD</b> GK <b>G</b> VF <b>ANDGE</b> LV <b>SAV</b> Q <b>VHP</b> Y <b>FW</b> Y <b>SG</b> CV <b>EP</b> PP <b>S</b>	C5
AF068748_EXT-2	DCPYL <b>YYPV</b> AK <b>EL</b> EP <b>KD</b> GK <b>G</b> VF <b>ANDGE</b> LV <b>SAV</b> Q <b>VHP</b> Y <b>FW</b> Y <b>SG</b> CV <b>EP</b> PP <b>S</b>	
Q06147	LQPEVLS <b>KIL</b> AK <b>FI</b> PK <b>LG</b> NG <b>IF</b> SWD <b>GK</b> FP <b>LE</b> PE <b>VE</b> IM <b>PR</b> CK <b>TL</b> LR-----	
Q12246	LEPEVLS <b>KIL</b> AK <b>FI</b> PK <b>Y</b> ES <b>G</b> IF <b>SWD</b> G <b>K</b> FP <b>LE</b> PE <b>VE</b> IM <b>PM</b> CK <b>TL</b> LR-----	
Q14159	YSKHLNY <b>KVR</b> SR <b>FT</b> P <b>YNTG</b> K <b>RY</b> F <b>AD</b> GES <b>Y</b> PLE <b>PF</b> CR <b>VAP</b> K <b>GT</b> TL <b>SP</b> -----V	
Q18425	D <b>LF</b> FK <b>H</b> EV <b>S</b> SM <b>EE</b> V <b>S</b> EG <b>S</b> H <b>V</b> ED <b>GE</b> Y <b>DT</b> KT <b>IF</b> AST <b>K</b> N <b>HI</b> S <b>VS</b> STA-----	
SPkinasemHSDA59H18	GKKRFG <b>IC</b> SS <b>HP</b> SCC <b>T</b> Y <b>SNS</b> SW <b>NC</b> D <b>GE</b> Y <b>HS</b> PA <b>IE</b> VR <b>VHC</b> Q <b>Y</b> RL <b>F</b> AR-----	
corrected_human_sphingosine	WKPOQMPPPEEPL	
AF068748_EXT-2	RDSRRGPPPEEP	
Q06147	-NGRYDTDFDSM	
Q12246	-NGRYDTDFDSM	
Q14159	AGFQLLDI-----	
Q18425	-----	
SPkinasemHSDA59H18	-GIEENPKPDSHS	

FIG. 4

PHYLIP - Protein Distance Analysis

Sequences analyzed:

- 1. SPkinaseinHSDA59H18
- 2. Q18425
- 3. O14159
- 4. Q06147
- 5. Q12246
- 6. coorrected\_human\_sphingosine
- 7. AF068748\_EXT-2

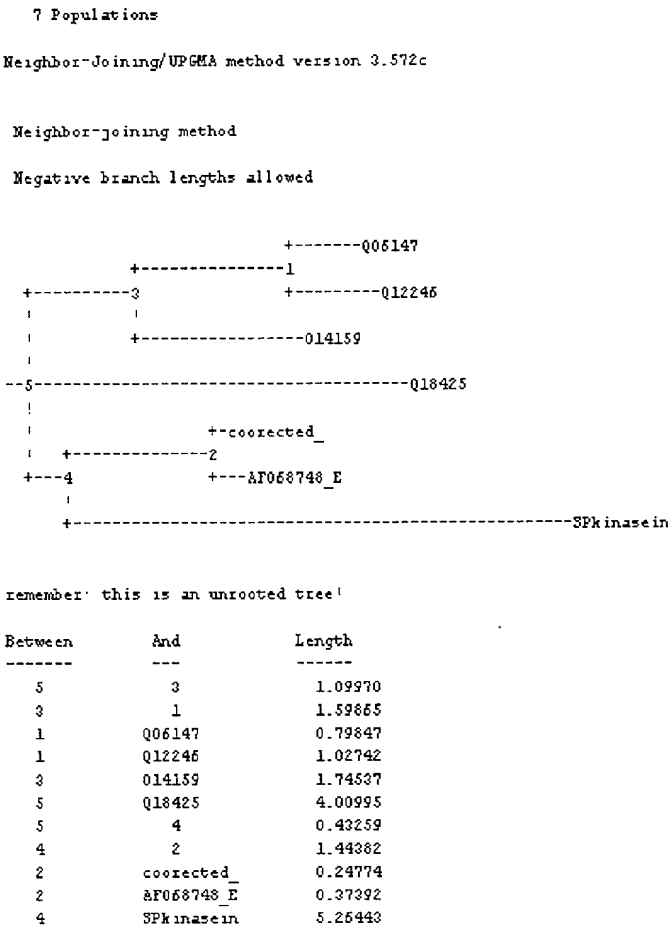


FIG. 5

Multiple Alignment:

80432911	AGAPGADACSVPVSEIIAVEETDVHGKHQSGKWQKMEKPYAFTVHCVKRAERHRWKWAQ
SPkinaseinHSDA59H18	-----MEKPYAFTVHCVKRAERHRWKWAQ
80432911	WTFWCPEEQQLCHLWQLTREMLEKLTSEPKHLLVFINPFGKGQGGKRIYERKVAPLFTLA
SPkinaseinHSDA59H18	WTFWCPEEQQLCHLWQLTREMLEKLTSEPKHLLVFINPFGKGQGGKRIYERKVAPLFTLA
80432911	SITTDII-----TEHANQAKETLYEINIDKYDGIVCVGGDGMFSEVLHGLIGR
SPkinaseinHSDA59H18	SITTDIIIGNKFFYN YVEVTEHANQAKETLYEINIDKYDGIVCVGGDGMFSEVLHGLIGR
80432911	TQRSAGVDQNHPR-----
SPkinaseinHSDA59H18	TQRSAGVDQNHPR A VLPSSLRIGIIPAGSTDCVCYSTWGTSDAETSALHIWVGDSLAMD
80432911	-----VSSVHHNSTLLRYSVSLGGYGFYVDI IKDSEKKRWLGLARYDFSGLKTFLSHHCYEGTVS
SPkinaseinHSDA59H18	-----FLPAQHTVGSPEDRKPCRAGCFVCRQSKQQLLEE QKKALYGLEAAEDVEEWQVWVGKFLA
80432911	-----INATNMSCACRES P RGLSPA AHLGDSSDL ILIRKCSR FNFLRFLIRHTNQDQDFDFTFY
SPkinaseinHSDA59H18	-----EYVRVKKFFQTSKHMEDEDS DLKEGKKRFGHI CSSHPSCCCTVSNSSWNC DGEVLHSP A
80432911	-----IEVRVHCQLVELFA RGIENPKPDSHS
SPkinaseinHSDA59H18	-----